

Fig. 1

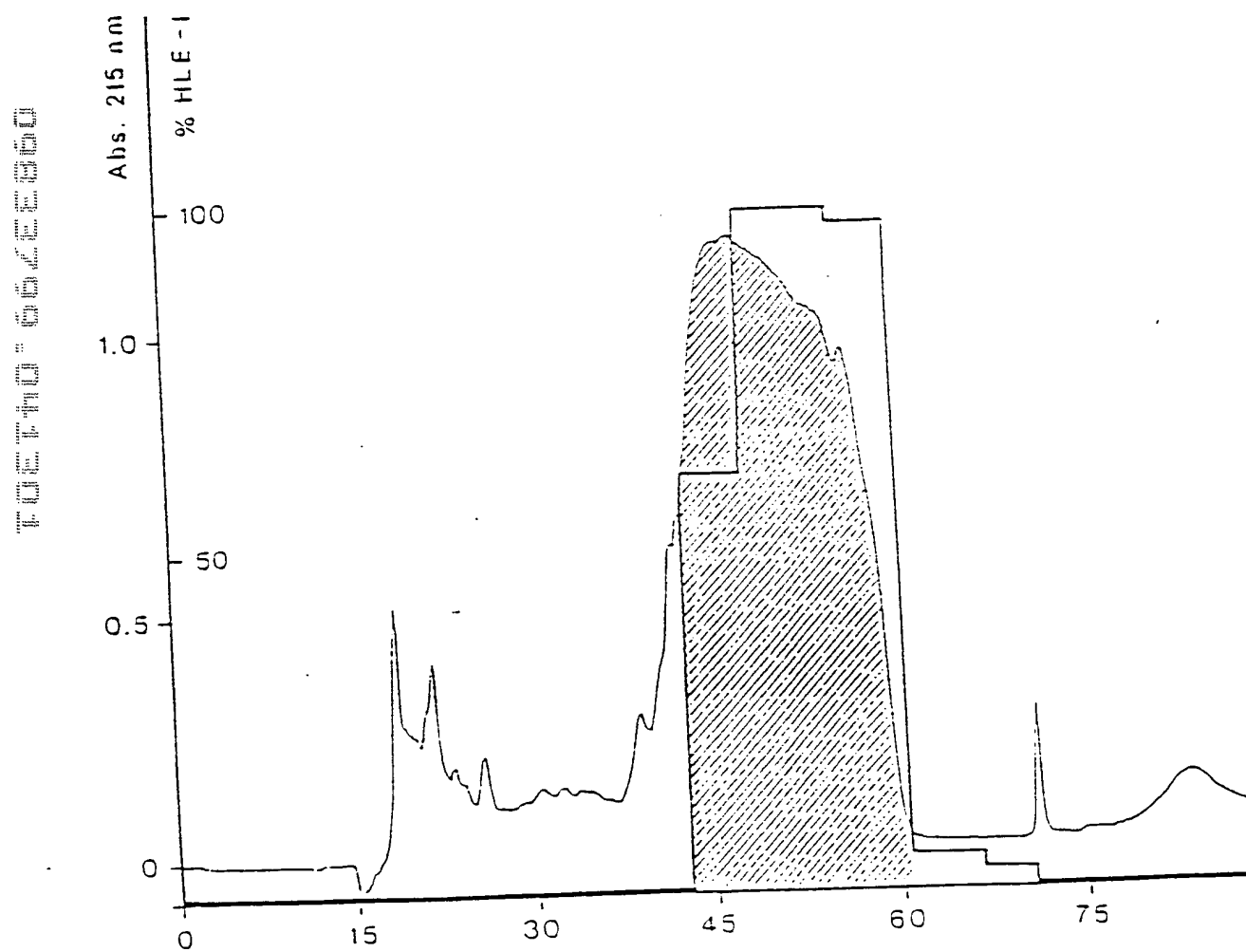


Fig. 2

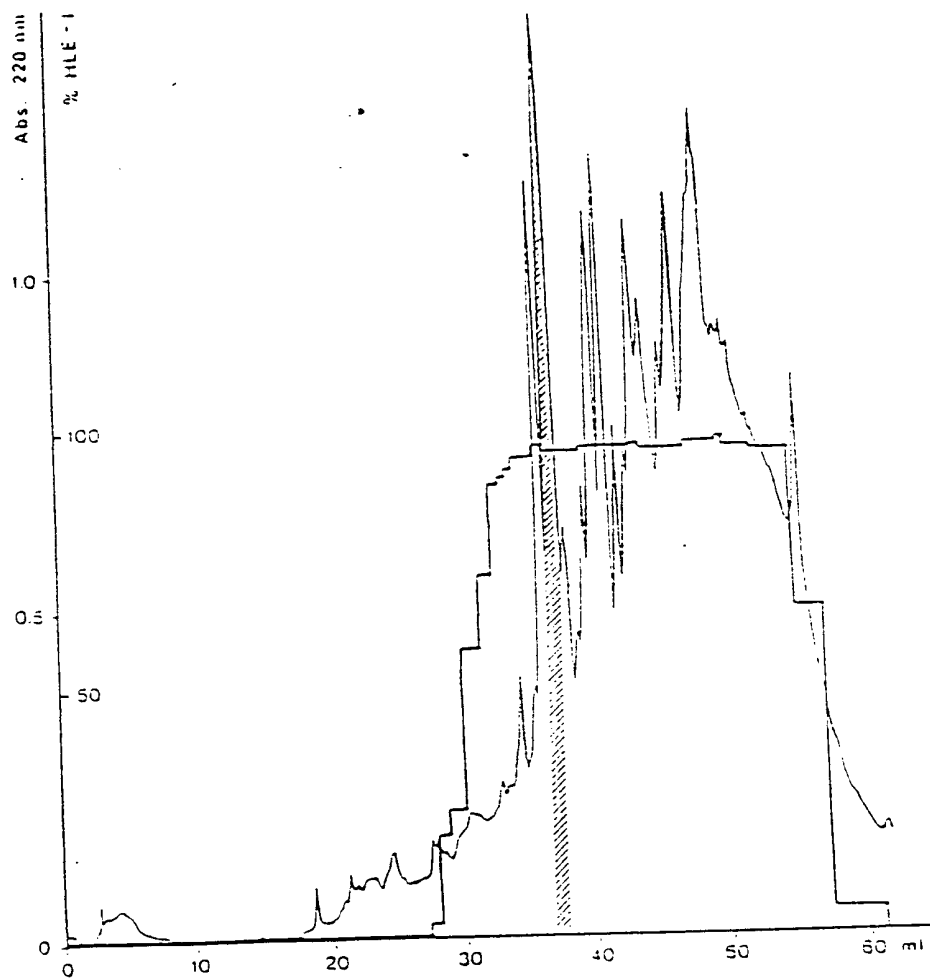


Fig. 3

09833799.044304

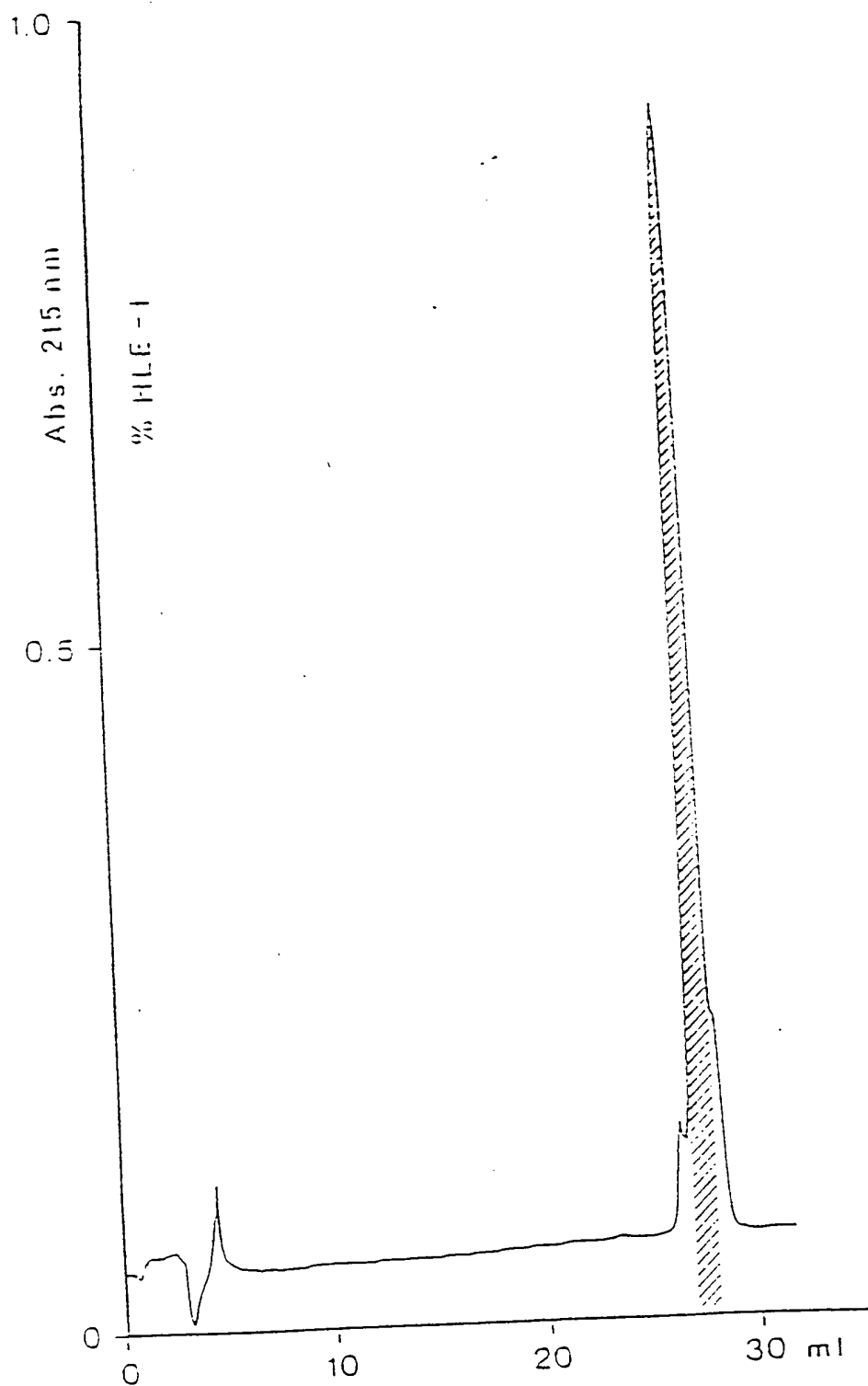


Fig. 4

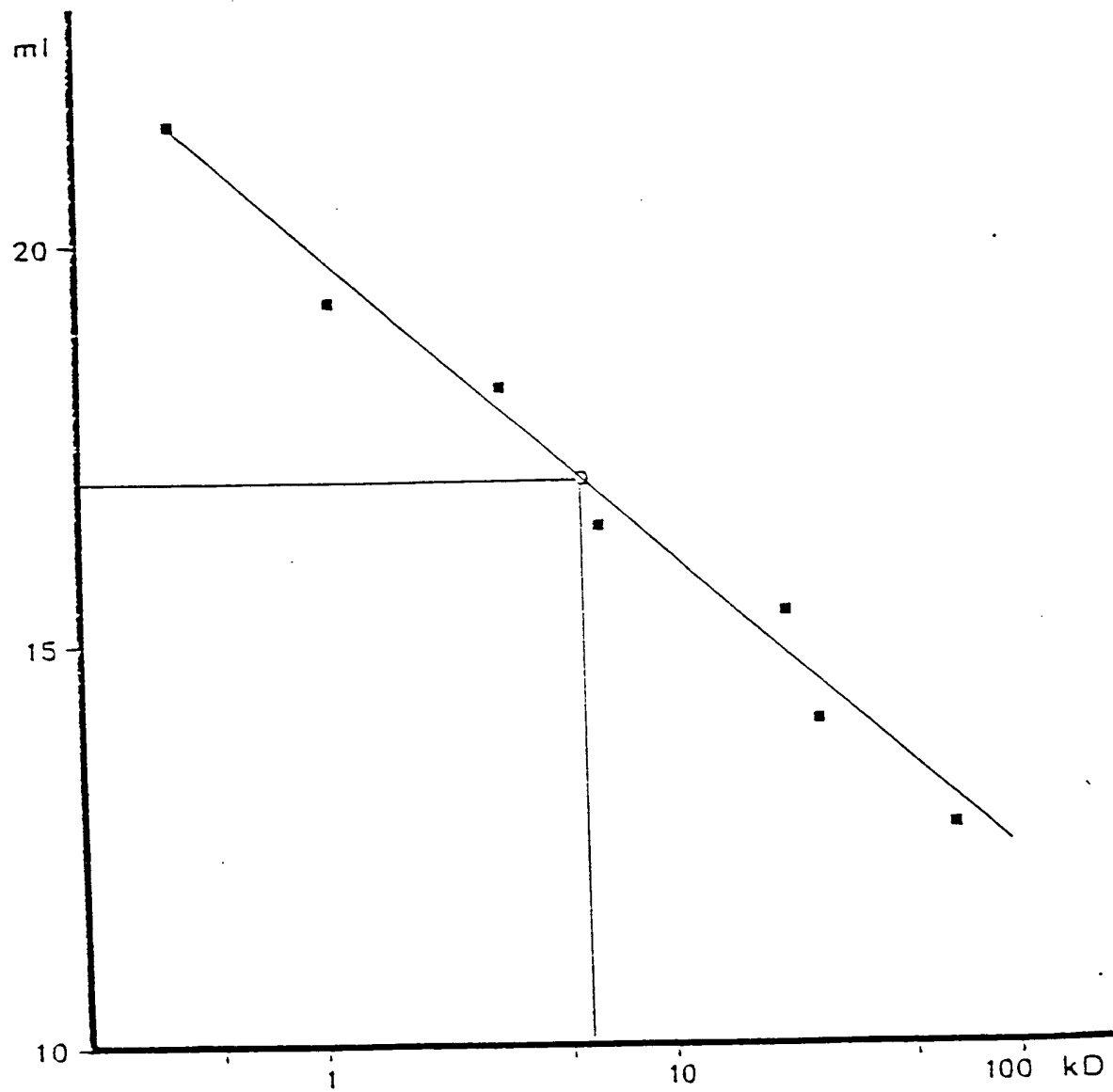


Fig. 5

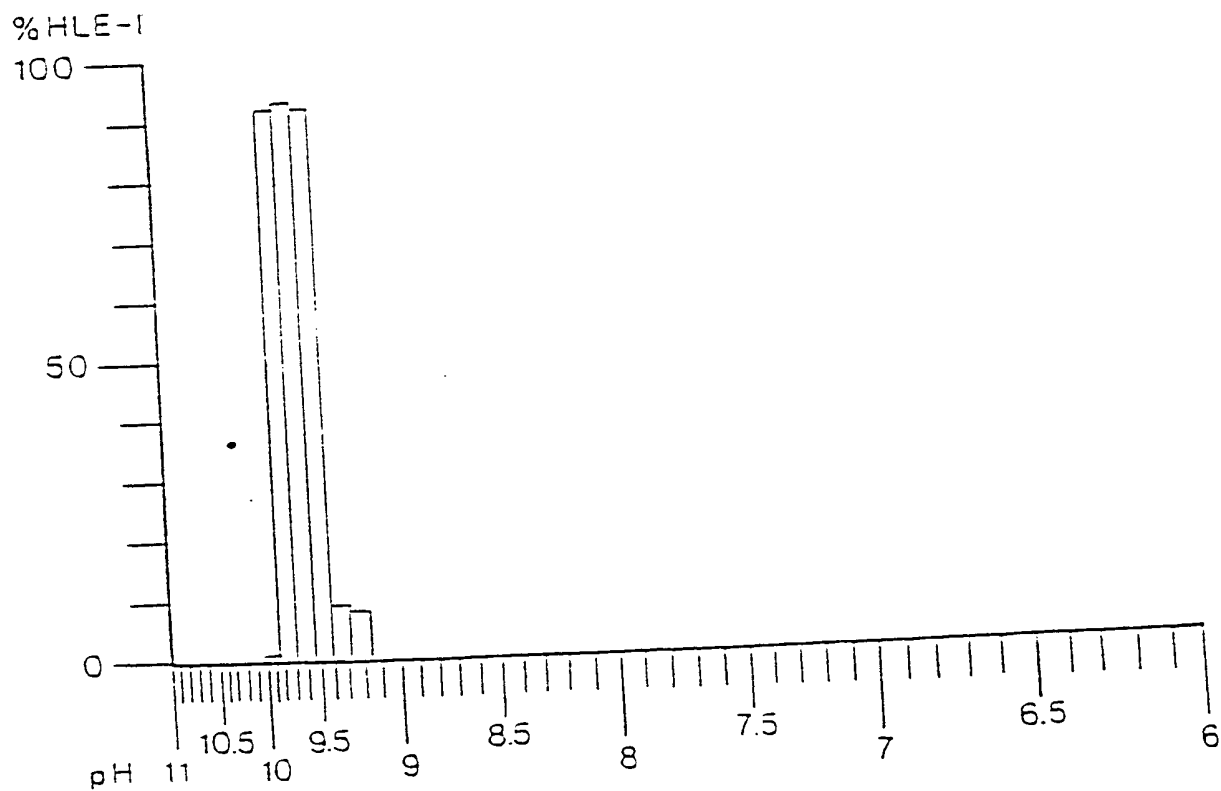
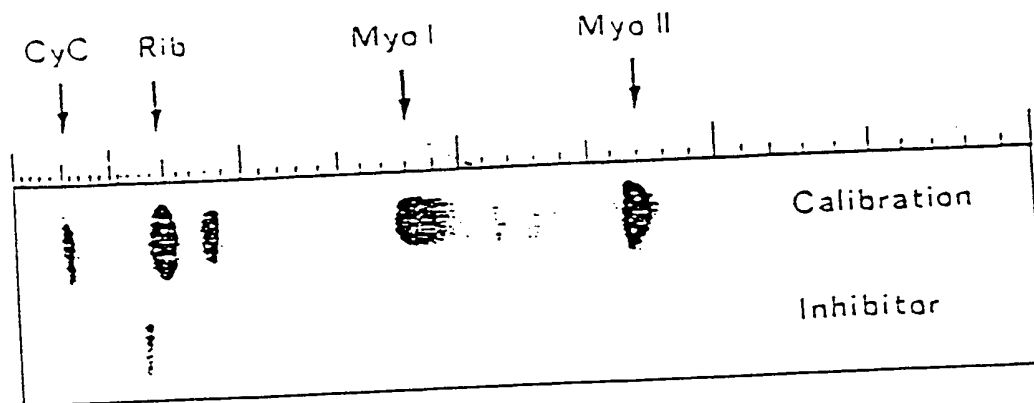


Fig. 6

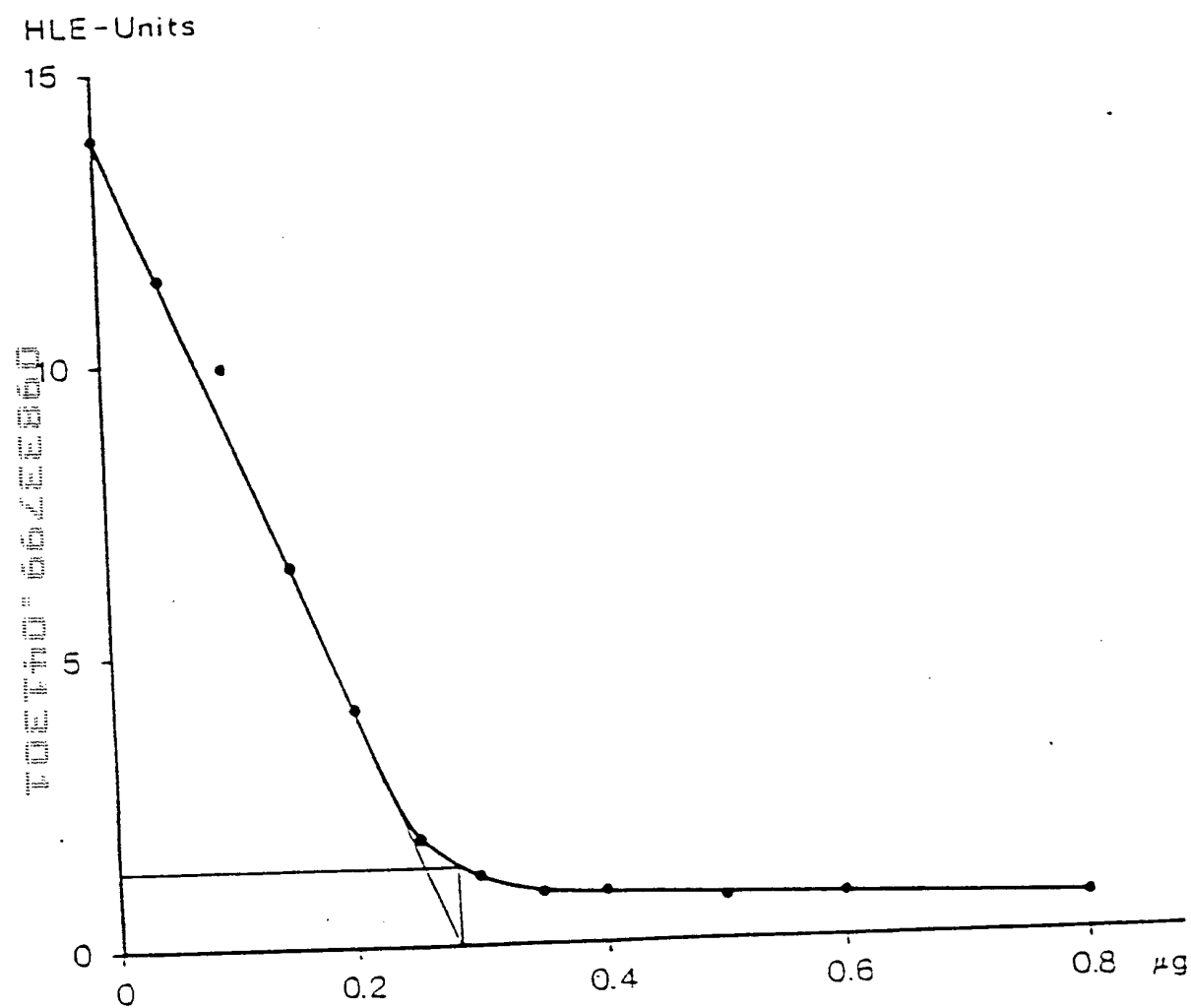


Fig. 7

FIGURE 8

PROTEIN SEQUENCE OF ELASTASE INHIBITOR



X=UNIDENTIFIED T=TRYPTIC FRAGMENTS C=CHYMOTRYPTIC FRAGMENTS

TEETH 064E860

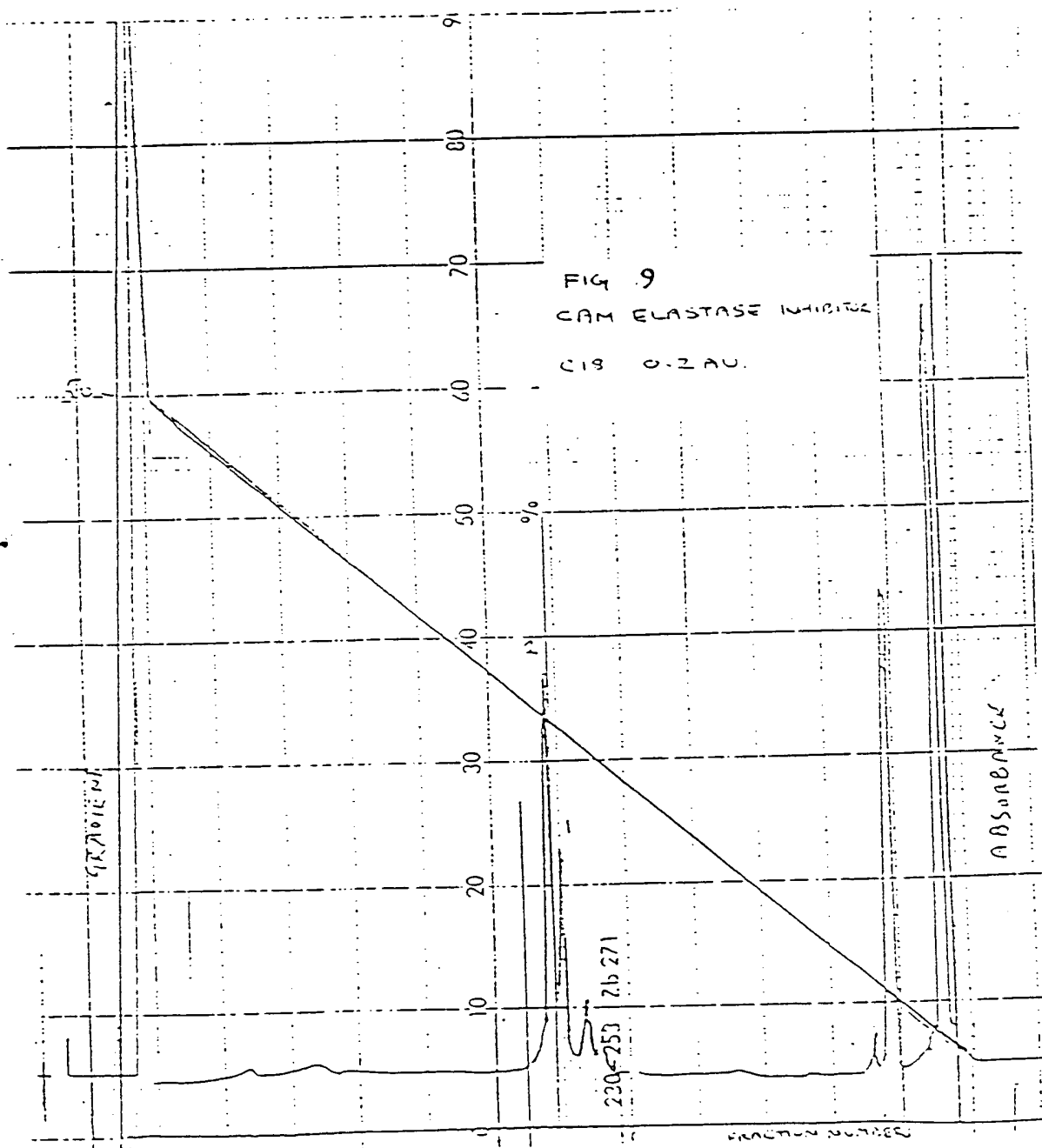


FIG 9.

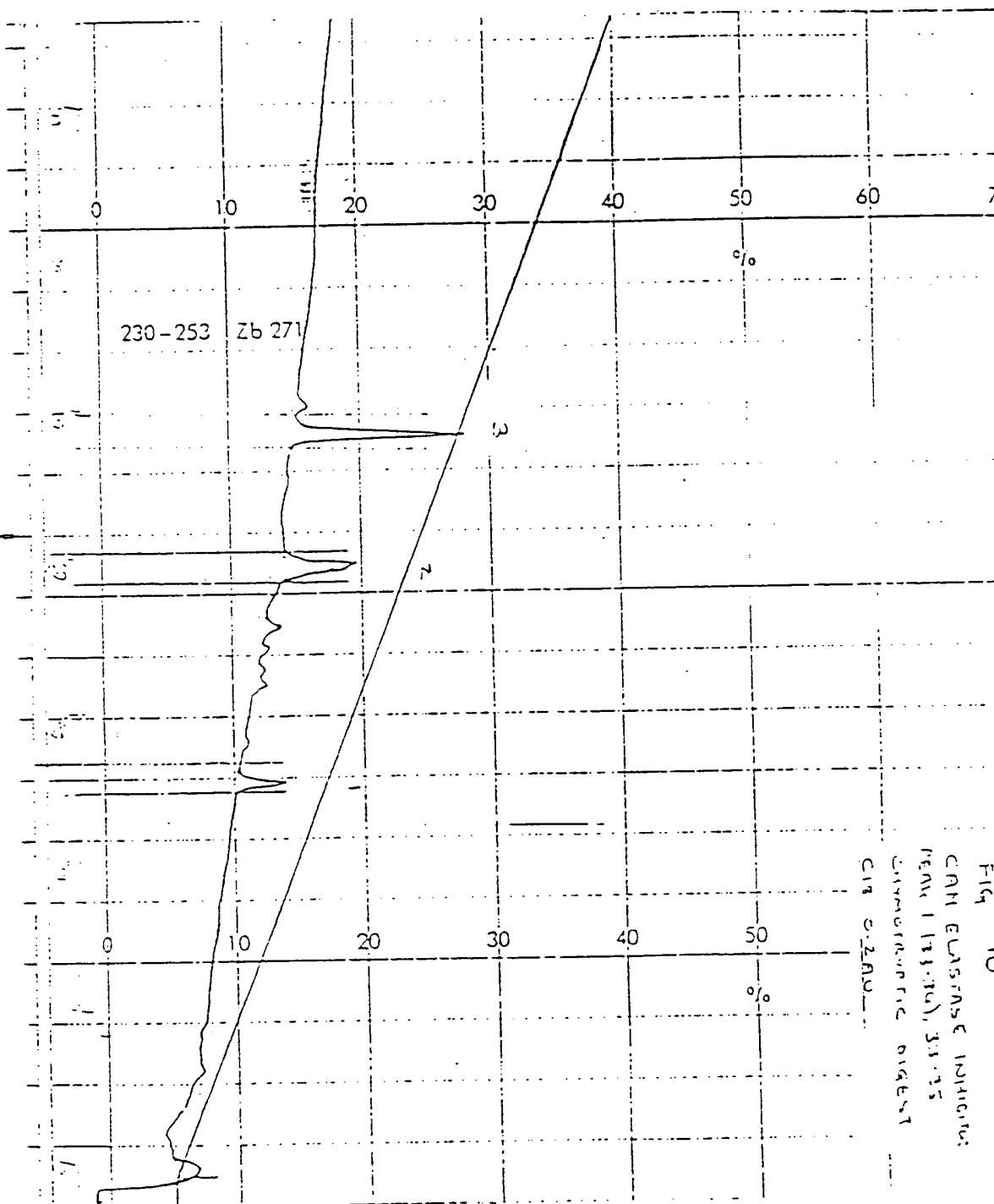
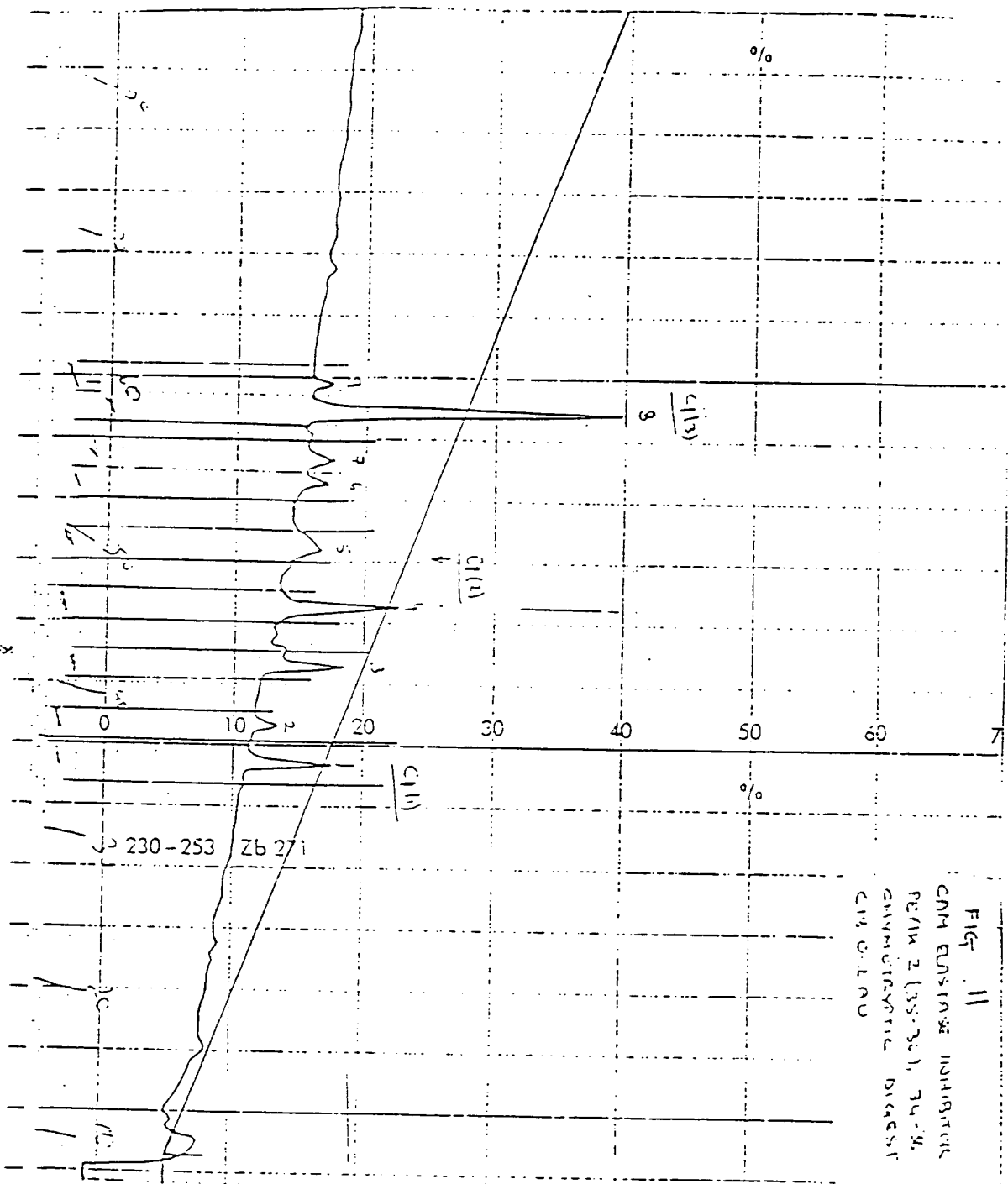
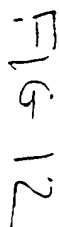


Fig 10
CNI ELASINS Indicator
PENN 1 (13.30), 33.75
CHROMATOPIC DIGEST
CIR 0.2000

00833799 044304

11
F16



AlaGlnGluProValLysGlyProValSerThr

1 ELI1
AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACT
GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGA

LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsnArg

63 ELI3
AAGCCAGGTTCTTGTCCTATTATCTTGATTGCTTGGCGCTATGTTAAACCCACCTAACCGT
TTCGGTCAAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCA
ELI2 ←

CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet

123 ELI5
TGTTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCTGCGGTATG
ACAACTTCTGTGACTTAACAGGTCCATAGTTTTTACGACACTTCCAAGGACGCCATAC
 ELI4 ←

AlaCysPheValProGlnEndEnd

183 GCTTGTTTCGTTCCACAATAATAG

CGAACAAAGCAAGGTGTTATTATCCTAG 210
 ELI6 ←

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC
5' DNA
Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln
TGC GGG ATG GCC TGT TTC GTT CCC CAG

Z = T, C or A

P = A or G

Figure 15

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
 GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC
 5' DNA
 Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
 CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln
 TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

GCCGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCACACTGTCCA
 TTCTTCCTCCCATTGAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACTTTCCAATAAAGAGTTCCG
 GAATTC

Poly A 3'
 signal

Z = T, C or A

P = A or G

TOE140-664EE660

10 30 50

GGAATTCCGGTTCCTCATCGCTGGGACGCTGGTTCTAGAGGCAGCTGTCACGGGAGTTCC

EcoRI XbaI

F L I A G T L V L E A A V T G V P

|-----IN-FRAME UPSTREAM PROTEIN SEQUENCE-----

70 90 110

TGTTAAAGGTCAAGACACTGTCAAAGGCCGTGTTCCATTCAATGGACAAGATCCCGTTAA

V K G Q D T V K G R V P F N G Q D P V K

130 150 170

AGGACAAGTTTCAGTTAAAGGTCAAGATAAAGTCAAAGCGCAAGAGCCAGTCAAAGGTCC

G Q V S V K G Q D K V K

AlaGlnGluProValLysGlyPr

|--ELASTASE INHIBITOR--

Cont'd 16b of 19

190

210

230

250

270

290

310

330

350

370

390

410

430

450

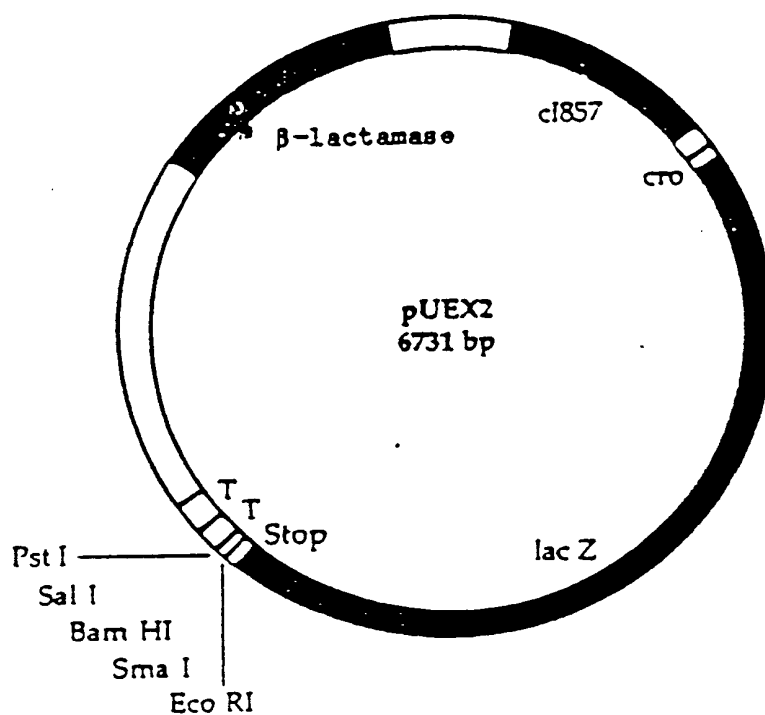
470

490

Poly A

EcoRI

signal



EcoRI SmaI BamHI SalI PstI
 | | | | |
 pUEX2 GAA TTC CCG GGG ATC CGT CGA CCT GCA GCC AAG CTT GCT GAT TGA
 Glu Phe Pro Gly Ile Arg Arg Pro Ala Ala Lys Leu Ala Asp ***

FIG 17

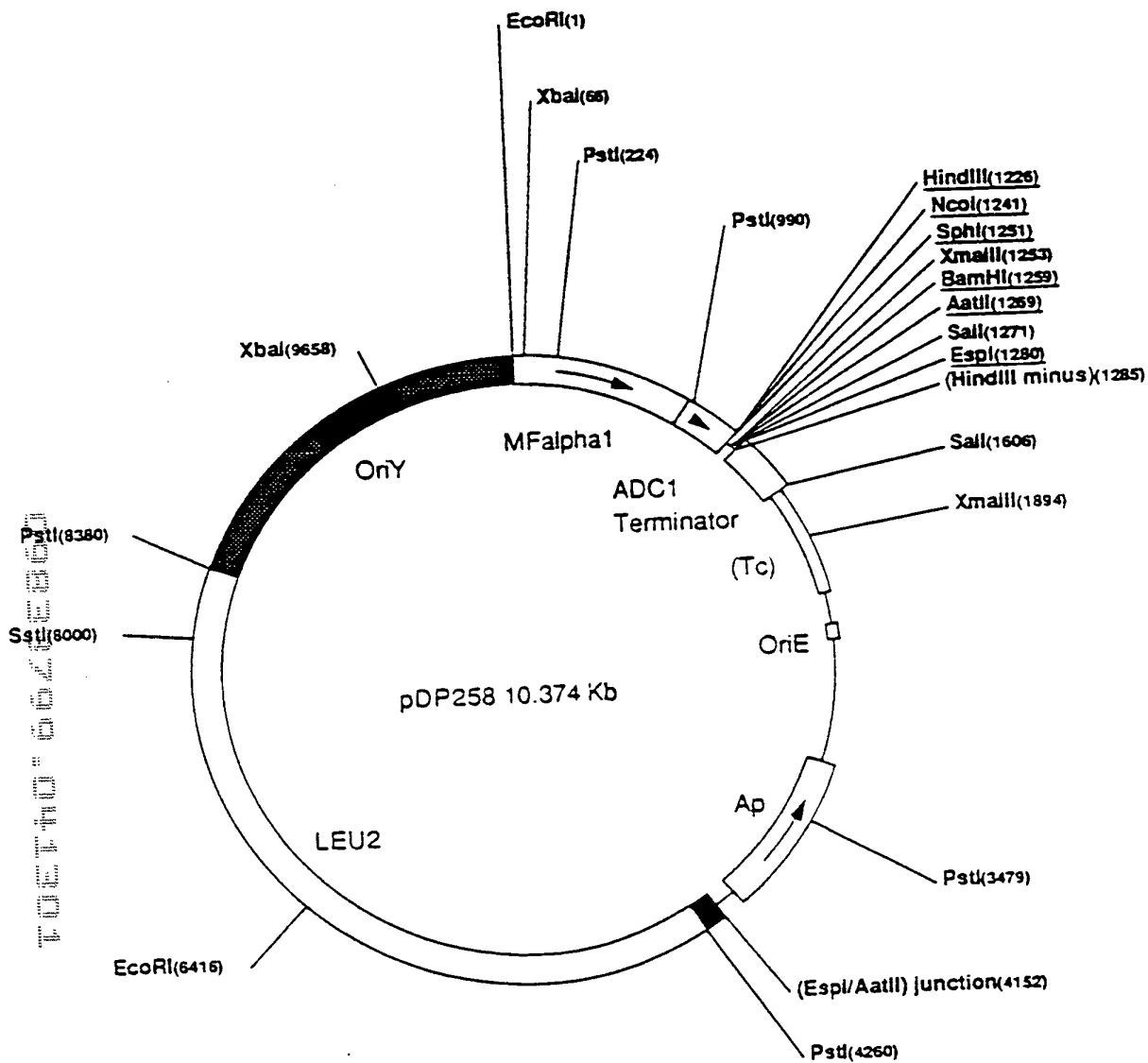


FIG 18

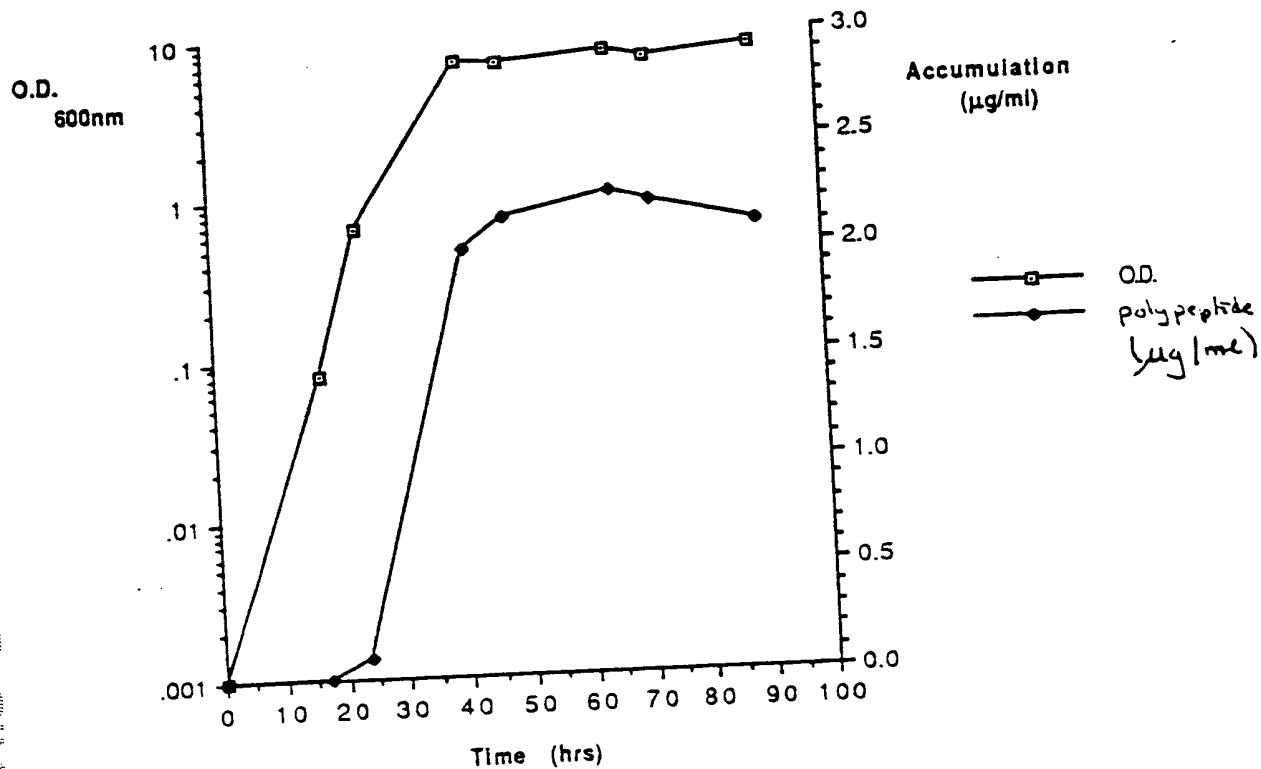


FIG 19